

ABSTRACT OF THE DISCLOSURE

A data processing system and method for managing and presenting information derived from a differential expression of genetic information which can be used to model a physiological response of biological cells. A data-represented map of metabolic pathways is provided. The map has a matrix of regions and locations within each of the regions. The regions are defined by respective coordinate sets. Each of the metabolic pathways include, at certain ones of the locations, respective graphical representations of a reaction, a substrate and a product of the reaction, and at least one biological catalyst of the reaction. An association mechanism links previously generated sets of affected sequence data to biological catalyst identifiers, each identifying one or more unique biological catalysts, and which links the biological catalyst identifiers to the coordinate sets. The sets of affected sequence data represent a direction and a magnitude of regulation of each one of a number of different nucleic acid sequences.